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Emergence of TEM, SHV, and CTX-M-extended spectrum β-lactamases and class 1 integron among Enterobacter cloacae isolates collected from hospitals of Tehran and Qazvin, Iran.

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Abstract

Extended-spectrum β-lactamase (ESBL) production is an important resistance mechanism among clinical isolates of Enterobacter cloacae. TEM, SHV, and CTX-M are the most common ESBL genotypes among Enterobacter spp. The main aims of this study were to determine the antimicrobial susceptibility pattern and to detect ESBL-encoding genes as well as intI1 genes. One hundred twenty isolates of E. cloacae were collected from hospitals of Tehran and Qazvin, Iran. The isolates were identified by standard laboratory methods and API 20E strips. ESBL screening was performed by the combined disk method. PCR and sequencing were conducted for detection of ESBL-encoding genes as well as intI1 genes. Clonal relatedness of ESBL-producing isolates was assessed by the enterobacterial repetitive intergenic consensus (ERIC)-PCR method. Of 120 isolates, 57 (47.5%) were characterized as multidrug resistant among those 48 (84.2%) isolates carried class 1 integron. Fifty-three (44.2%) isolates were found to be ESBL producers, in which bla(CTX-M-15) (60.4%) was the most common gene followed by bla(TEM-1) (32.1%), bla(TEM-169) (13.2%), and bla(SHV-12) (7.5%) either alone or in combination. Forty-four of the 53 (83.01%) ESBL-producing isolates were genetically unrelated. For the first time, this study describes the emergence of TEM-169, SHV-12, and CTX-M-15 ESBL genotypes in E. cloacae isolates in Iran.

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